

1/6

Fig. 1a.1

GCGGCCTGGC TACCGCGCGC TCCGGAGGCC ATG CGG GCG TTG GCG CAG CGC AGC
 Met Arg Ala Leu Ala Gln Arg Ser
 -27 -25 -20

GAC CGG CGG CTG CTG CTG CTT GTT GTT TTG TCA GTA ATG ATT CTT GAG
 Asp Arg Arg Leu Leu Leu Leu Val Val Leu Ser Val Met Ile Leu Glu
 -15 -10 -5

ACC GTT ACA AAC CAA GAC CTG CCT GTG ATC AAG TGT GTT TTA ATC AGT
 Thr Val Thr Asn Gln Asp Leu Pro Val Ile Lys Cys Val Leu Ile Ser
 1 5 10

CAT GAG AAC AAT GGC TCA TCA GCG GGA AAG CCA TCA TCG TAC CGA ATG
 His Glu Asn Asn Gly Ser Ser Ala Gly Lys Pro Ser Ser Tyr Arg Met
 15 20 25

GTG CGA GGA TCC CCA GAA GAC CTC CAG TGT ACC CCG AGG CGC CAG AGT
 Val Arg Gly Ser Pro Glu Asp Leu Gln Cys Thr Pro Arg Arg Gln Ser
 30 35 40 45

GAA GGG ACG GTA TAT GAA GCG GCC ACC GTG GAG GTG GCC GAG TCT GGG
 Glu Gly Thr Val Tyr Glu Ala Ala Thr Val Glu Val Ala Glu Ser Gly
 50 55 60

TCC ATC ACC CTG CAA GTG CAG CTC GCC ACC CCA GGG GAC CTT TCC TGC
 Ser Ile Thr Leu Gln Val Gln Leu Ala Thr Pro Gly Asp Leu Ser Cys
 65 70 75

CTC TGG GTC TTT AAG CAC AGC TCC CTG GGC TGC CAG CCG CAC TTT GAT
 Leu Trp Val Phe Lys His Ser Ser Leu Gly Cys Gln Pro His Phe Asp
 80 85 90

TTA CAA AAC AGA GGA ATC GTT TCC ATG GCC ATC TTG AAC GTG ACA GAG
 Leu Gln Asn Arg Gly Ile Val Ser Met Ala Ile Leu Asn Val Thr Glu
 95 100 105

ACC CAG GCA GGA GAA TAC CTA CTC CAT ATT CAG AGC GAA CGC GCC AAC
 Thr Gln Ala Gly Glu Tyr Leu Leu His Ile Gln Ser Glu Arg Ala Asn
 110 115 120 125

TAC ACA GTA CTG TTC ACA GTG AAT GTA AGA GAT ACA CAG CTG TAT GTG
 Tyr Thr Val Leu Phe Thr Val Asn Val Arg Asp Thr Gln Leu Tyr Val
 130 135 140

CTA AGG AGA CCT TAC TTT AGG AAG ATG GAA AAC CAG GAT GCA CTG CTC
 Leu Arg Arg Pro Tyr Phe Arg Lys Met Glu Asn Gln Asp Ala Leu Leu
 145 150 155

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Fig. 1a.2

TGC	ATC	TCC	GAG	GGT	GTT	CCG	GAG	CCC	ACT	GTG	GAG	TGG	GTG	CTC	TGC	
Cys	Ile	Ser	Glu	Gly	Val	Pro	Glu	Pro	Thr	Val	Glu	Trp	Val	Leu	Cys	
		160					165					170				
AGC	TCC	CAC	AGG	GAA	AGC	TGT	AAA	GAA	GAA	GGC	CCT	GCT	GTT	GTC	AGA	
Ser	Ser	His	Arg	Glu	Ser	Cys	Lys	Glu	Glu	Gly	Pro	Ala	Val	Val	Arg	
		175				180					185					
AAG	GAG	GAA	AAG	GTA	CTT	CAT	GAG	TTG	TTC	GGA	ACA	GAC	ATC	AGA	TGC	
Lys	Glu	Glu	Lys	Val	Leu	His	Glu	Leu	Phe	Gly	Thr	Asp	Ile	Arg	Cys	
		190			195					200					205	
TGT	GCT	AGA	AAT	GCA	CTG	GGC	CGC	GAA	TGC	ACC	AAG	CTG	TTC	ACC	ATA	
Cys	Ala	Arg	Asn	Ala	Leu	Gly	Arg	Glu	Cys	Thr	Lys	Leu	Phe	Thr	Ile	
				210					215					220		
GAT	CTA	AAC	CAG	GCT	CCT	CAG	AGC	ACA	CTG	CCC	CAG	TTA	TTC	CTG	AAA	
Asp	Leu	Asn	Gln	Ala	Pro	Gln	Ser	Thr	Leu	Pro	Gln	Leu	Phe	Leu	Lys	
			225					230					235			
GTG	GGG	GAA	CCC	TTG	TGG	ATC	AGG	TGT	AAG	GCC	ATC	CAT	GTG	AAC	CAT	
Val	Gly	Glu	Pro	Leu	Trp	Ile	Arg	Cys	Lys	Ala	Ile	His	Val	Asn	His	
		240					245					250				
GGA	TTC	GGG	CTC	ACC	TGG	GAG	CTG	GAA	GAC	AAA	GCC	CTG	GAG	GAG	GGC	
Gly	Phe	Gly	Leu	Thr	Trp	Glu	Leu	Glu	Asp	Lys	Ala	Leu	Glu	Glu	Gly	
		255				260					265					
AGC	TAC	TTT	GAG	ATG	AGT	ACC	TAC	TCC	ACA	AAC	AGG	ACC	ATG	ATT	CGG	
Ser	Tyr	Phe	Glu	Met	Ser	Thr	Tyr	Ser	Thr	Asn	Arg	Thr	Met	Ile	Arg	
					275					280					285	
ATT	CTC	TTG	GCC	TTT	GTG	TCT	TCC	GTG	GGA	AGG	AAC	GAC	ACC	GGA	TAT	
Ile	Leu	Leu	Ala	Phe	Val	Ser	Ser	Val	Gly	Arg	Asn	Asp	Thr	Gly	Tyr	
				290					295					300		
TAC	ACC	TGC	TCT	TCC	TCA	AAG	CAC	CCC	AGC	CAG	TCA	GCG	TTG	GTG	ACC	
Tyr	Thr	Cys	Ser	Ser	Ser	Lys	His	Pro	Ser	Gln	Ser	Ala	Leu	Val	Thr	
				305				310					315			
ATC	CTA	GAA	AAA	GGG	TTT	ATA	AAC	GCT	ACC	AGC	TCG	CAA	GAA	GAG	TAT	
Ile	Leu	Glu	Lys	Gly	Phe	Ile	Asn	Ala	Thr	Ser	Ser	Gln	Glu	Glu	Tyr	
		320					325					330				
GAA	ATT	GAC	CCG	TAC	GAA	AAG	TTC	TGC	TTC	TCA	GTC	AGG	TTT	AAA	GCG	
Glu	Ile	Asp	Pro	Tyr	Glu	Lys	Phe	Cys	Phe	Ser	Val	Arg	Phe	Lys	Ala	
		335				340					345					

Fig. 1a.3

TAC	CCA	CGA	ATC	CGA	TGC	ACG	TGG	ATC	TTC	TCT	CAA	GCC	TCA	TTT	CCT	
Tyr	Pro	Arg	Ile	Arg	Cys	Thr	Trp	Ile	Phe	Ser	Gln	Ala	Ser	Phe	Pro	
350					355					360					365	
TGT	GAA	CAG	AGA	GGC	CTG	GAG	GAT	GGG	TAC	AGC	ATA	TCT	AAA	TTT	TGC	
Cys	Glu	Gln	Arg	Gly	Leu	Glu	Asp	Gly	Tyr	Ser	Ile	Ser	Lys	Phe	Cys	
				370					375						380	
GAT	CAT	AAG	AAC	AAG	CCA	GGA	GAG	TAC	ATA	TTC	TAT	GCA	GAA	AAT	GAT	
Asp	His	Lys	Asn	Lys	Pro	Gly	Glu	Tyr	Ile	Phe	Tyr	Ala	Glu	Asn	Asp	
			385					390					395			
GAC	GCC	CAG	TTC	ACC	AAA	ATG	TTC	ACG	CTG	AAT	ATA	AGA	AAG	AAA	CCT	
Asp	Ala	Gln	Phe	Thr	Lys	Met	Phe	Thr	Leu	Asn	Ile	Arg	Lys	Lys	Pro	
		400					405					410				
CAA	GTG	CTA	GCA	AAT	GCC	TCA	GCC	AGC	CAG	GCG	TCC	TGT	TCC	TCT	GAT	
Gln	Val	Leu	Ala	Asn	Ala	Ser	Ala	Ser	Gln	Ala	Ser	Cys	Ser	Ser	Asp	
	415					420					425					
GGC	TAC	CCG	CTA	CCC	TCT	TGG	ACC	TGG	AAG	AAG	TGT	TCG	GAC	AAA	TCT	
Gly	Tyr	Pro	Leu	Pro	Ser	Trp	Thr	Trp	Lys	Lys	Cys	Ser	Asp	Lys	Ser	
430					435					440					445	
CCC	AAT	TGC	ACG	GAG	GAA	ATC	CCA	GAA	GGA	GTT	TGG	AAT	AAA	AAG	GCT	
Pro	Asn	Cys	Thr	Glu	Glu	Ile	Pro	Glu	Gly	Val	Trp	Asn	Lys	Lys	Ala	
				450					455					460		
AAC	AGA	AAA	GTG	TTT	GGC	CAG	TGG	GTG	TCG	AGC	AGT	ACT	CTA	AAT	ATG	
Asn	Arg	Lys	Val	Phe	Gly	Gln	Trp	Val	Ser	Ser	Ser	Thr	Leu	Asn	Met	
			465				470						475			
AGT	GAG	GCC	GGG	AAA	GGG	CTT	CTG	GTC	AAA	TGC	TGT	GCG	TAC	AAT	TCT	
Ser	Glu	Ala	Gly	Lys	Gly	Leu	Leu	Val	Lys	Cys	Cys	Ala	Tyr	Asn	Ser	
		480					485					490				
ATG	GGC	ACG	TCT	TGC	GAA	ACC	ATC	TTT	TTA	AAC	TCA	CCA	GGC	CCC	TTC	
Met	Gly	Thr	Ser	Cys	Glu	Thr	Ile	Phe	Leu	Asn	Ser	Pro	Gly	Pro	Phe	
	495					500					505					
CCT	TTC	ATC	CAA	GAC	AAC	ATC	TCC	TTC	TAT	GCG	ACC	ATT	GGG	CTC	TGT	
Pro	Phe	Ile	Gln	Asp	Asn	Ile	Ser	Phe	Tyr	Ala	Thr	Ile	Gly	Leu	Cys	
510					515					520					525	
CTC	CCC	TTC	ATT	GTT	GTT	CTC	ATT	GTG	TTG	ATC	TGC	CAC	AAA	TAC	AAA	
Leu	Pro	Phe	Ile	Val	Val	Leu	Ile	Val	Leu	Ile	Cys	His	Lys	Tyr	Lys	
				530					535					540		

Fig. 1a.4

AAG	CAA	TTT	AGG	TAC	GAG	AGT	CAG	CTG	CAG	ATG	ATC	CAG	GTG	ACT	GGC			
Lys	Gln	Phe	Arg	Tyr	Glu	Ser	Gln	Leu	Gln	Met	Ile	Gln	Val	Thr	Gly	545	550	555
CCC	CTG	GAT	AAC	GAG	TAC	TTC	TAC	GTT	GAC	TTC	AGG	GAC	TAT	GAA	TAT			
Pro	Leu	Asp	Asn	Glu	Tyr	Phe	Tyr	Val	Asp	Phe	Arg	Asp	Tyr	Glu	Tyr	560	565	570
GAC	CTT	AAG	TGG	GAG	TTC	CCG	AGA	GAG	AAC	TTA	GAG	TTT	GGG	AAG	GTC			
Asp	Leu	Lys	Trp	Glu	Phe	Pro	Arg	Glu	Asn	Leu	Glu	Phe	Gly	Lys	Val	575	580	585
CTG	GGG	TCT	GGC	GCT	TTC	GGG	AGG	GTG	ATG	AAC	GCC	ACG	GCC	TAT	GGC			
Leu	Gly	Ser	Gly	Ala	Phe	Gly	Arg	Val	Met	Asn	Ala	Thr	Ala	Tyr	Gly	590	595	600
ATT	AGT	AAA	ACG	GGA	GTC	TCA	ATT	CAG	GTG	GCG	GTG	AAG	ATG	CTA	AAA			
Ile	Ser	Lys	Thr	Gly	Val	Ser	Ile	Gln	Val	Ala	Val	Lys	Met	Leu	Lys	610	615	620
GAG	AAA	GCT	GAC	AGC	TGT	GAA	AAA	GAA	GCT	CTC	ATG	TCG	GAG	CTC	AAA			
Glu	Lys	Ala	Asp	Ser	Cys	Glu	Lys	Glu	Ala	Leu	Met	Ser	Glu	Leu	Lys	625	630	635
ATG	ATG	ACC	CAC	CTG	GGA	CAC	CAT	GAC	AAC	ATC	GTG	AAT	CTG	CTG	GGG			
Met	Met	Thr	His	Leu	Gly	His	His	Asp	Asn	Ile	Val	Asn	Leu	Leu	Gly	640	645	650
GCA	TGC	ACA	CTG	TCA	GGG	CCA	GTG	TAC	TTG	ATT	TTT	GAA	TAT	TGT	TGC			
Ala	Cys	Thr	Leu	Ser	Gly	Pro	Val	Tyr	Leu	Ile	Phe	Glu	Tyr	Cys	Cys	655	660	665
TAT	GGT	GAC	CTC	CTC	AAC	TAC	CTA	AGA	AGT	AAA	AGA	GAG	AAG	TTT	CAC			
Tyr	Gly	Asp	Leu	Leu	Asn	Tyr	Leu	Arg	Ser	Lys	Arg	Glu	Lys	Phe	His	670	675	680
AGG	ACA	TGG	ACA	GAG	ATT	TTT	AAG	GAA	CAT	AAT	TTC	AGT	TCT	TAC	CCT			
Arg	Thr	Trp	Thr	Glu	Ile	Phe	Lys	Glu	His	Asn	Phe	Ser	Ser	Tyr	Pro	690	695	700
ACT	TTC	CAG	GCA	CAT	TCA	AAT	TCC	AGC	ATG	CCT	GGT	TCA	CGA	GAA	GTT			
Thr	Phe	Gln	Ala	His	Ser	Asn	Ser	Ser	Met	Pro	Gly	Ser	Arg	Glu	Val	705	710	715
CAG	TTA	CAC	CCG	CCC	TTG	GAT	CAG	CTC	TCA	GGG	TTC	AAT	GGG	AAT	TCA			
Gln	Leu	His	Pro	Pro	Leu	Asp	Gln	Leu	Ser	Gly	Phe	Asn	Gly	Asn	Ser	720	725	730

Fig. 1a.5

ATT CAT TCT GAA GAT GAG ATT GAA TAT GAA AAC CAG AAG AGG CTG GCA
 Ile His Ser Glu Asp Glu Ile Glu Tyr Glu Asn Gln Lys Arg Leu Ala
 735 740 745

GAA GAA GAG GAG GAA GAT TTG AAC GTG CTG ACG TTT GAA GAC CTC CTT
 Glu Glu Glu Glu Glu Asp Leu Asn Val Leu Thr Phe Glu Asp Leu Leu
 750 755 760 765

TGC TTT GCG TAC CAA GTG GCC AAA GGC ATG GAA TTC CTG GAG TTC AAG
 Cys Phe Ala Tyr Gln Val Ala Lys Gly Met Glu Phe Leu Glu Phe Lys
 770 775 780

TCG TGT GTC CAC AGA GAC CTG GCA GCC AGG AAT GTG TTG GTC ACC CAC
 Ser Cys Val His Arg Asp Leu Ala Ala Arg Asn Val Leu Val Thr His
 785 790 795

GGG AAG GTG GTG AAG ATC TGT GAC TTT GGA CTG GCC CGA GAC ATC CTG
 Gly Lys Val Val Lys Ile Cys Asp Phe Gly Leu Ala Arg Asp Ile Leu
 800 805 810

AGC GAC TCC AGC TAC GTC GTC AGG GGC AAC GCA CGG CTG CCG GTG AAG
 Ser Asp Ser Ser Tyr Val Val Arg Gly Asn Ala Arg Leu Pro Val Lys
 815 820 825

TGG ATG GCA CCC GAG AGC TTA TTT GAA GGG ATC TAC ACA ATC AAG AGT
 Trp Met Ala Pro Glu Ser Leu Phe Glu Gly Ile Tyr Thr Ile Lys Ser
 830 835 840 845

GAC GTC TGG TCC TAC GGC ATC CTT CTC TGG GAG ATA TTT TCA CTG GGT
 Asp Val Trp Ser Tyr Gly Ile Leu Leu Trp Glu Ile Phe Ser Leu Gly
 850 855 860

GTG AAC CCT TAC CCT GGC ATT CCT GTC GAC GCT AAC TTC TAT AAA CTG
 Val Asn Pro Tyr Pro Gly Ile Pro Val Asp Ala Asn Phe Tyr Lys Leu
 865 870 875

ATT CAG AGT GGA TTT AAA ATG GAG CAG CCA TTC TAT GCC ACA GAA GGG
 Ile Gln Ser Gly Phe Lys Met Glu Gln Pro Phe Tyr Ala Thr Glu Gly
 880 885 890

ATA TAC TTT GTA ATG CAA TCC TGC TGG GCT TTT GAC TCA AGG AAG CGG
 Ile Tyr Phe Val Met Gln Ser Cys Trp Ala Phe Asp Ser Arg Lys Arg
 895 900 905

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Fig. 1a.6

CCA TCC TTC CCC AAC CTG ACT TCA TTT TTA GGA TGT CAG CTG GCA GAG
 Pro Ser Phe Pro Asn Leu Thr Ser Phe Leu Gly Cys Gln Leu Ala Glu
 910 915 920 925

GCA GAA GAA GCA TGT ATC AGA ACA TCC ATC CAT CTA CCA AAA CAG GCG
 Ala Glu Glu Ala Cys Ile Arg Thr Ser Ile His Leu Pro Lys Gln Ala
 930 935 940

GCC CCT CAG CAG AGA GGC GGG CTC AGA GCC CAG TCG CCA CAG CGC CAG
 Ala Pro Gln Gln Arg Gly Gly Leu Arg Ala Gln Ser Pro Gln Arg Gln
 945 950 955

GTG AAG ATT CAC AGA GAA AGA AGT TAGCGAGGAG GCCTTGGACC CCGCCACCCT
 Val Lys Ile His Arg Glu Arg Ser
 960 965

AGCAGGCTGT AGACCGCAGA GCCAAGATTA GCCTCGCCTC TGAGGAAGCG CCCTACAGCG
 CGTTGCTTCG CTGGACTTTT CTCTAGATGC TGTCTGCCAT TACTCCAAAG TGACTTCTAT
 AAAATCAAAC CTCTCCTCGC ACAGGCGGGA GAGCCAATAA TGAGACTTGT TGGTGAGCCC
 GCCTACCCTG GGGGCCTTTC CACGAGCTTG AGGGGAAAGC CATGTATCTG AAATATAGTA
 TATTCTTGTA AATACGTGAA ACAAACCAAA CCCGTTTTTT GCTAAGGGAA AGCTAAATAT
 GATTTTAA AATCTATGTT TTAAATACT ATGTAACCTT TTCATCTATT TAGTGATATA
 TTTTATGGAT GGAAATAAAC TTTCTACTGT AAAAAAAAAA AAAAAAAAAA AAAAAA

Fig. 1b.1

CGAGGCGGCA TCCGAGGGCT GGGCCGGCGC CCTGGGGGAC CCCGGGCTCC GGAGGCC

ATG CCG GCG TTG GCG CGC GAC GCG GGC ACC GTG CCG CTG CTC GTT GTT
Met Pro Ala Leu Ala Arg Asp Ala Gly Thr Val Pro Leu Leu Val Val
-27 -25 -20 -15

TTT TCT GCA ATG ATA TTT GGG ACT ATT ACA AAT CAA GAT CTG CCT GTG
Phe Ser Ala Met Ile Phe Gly Thr Ile Thr Asn Gln Asp Leu Pro Val
-10 -5 1 5

ATC AAG TGT GTT TTA ATC AAT CAT AAG AAC AAT GAT TCA TCA GTG GGG
Ile Lys Cys Val Leu Ile Asn His Lys Asn Asn Asp Ser Ser Val Gly
10 15 20

AAG TCA TCA TCA TAT CCC ATG GTA TCA GAA TCC CCG GAA GAC CTC GGG
Lys Ser Ser Ser Tyr Pro Met Val Ser Glu Ser Pro Glu Asp Leu Gly
25 30 35

TGT GCG TTG AGA CCC CAG AGC TCA GGG ACA GTG TAC GAA GCT GCC GCT
Cys Ala Leu Arg Pro Gln Ser Ser Gly Thr Val Tyr Glu Ala Ala Ala
40 45 50

GTG GAA GTG GAT GTA TCT GCT TCC ATC ACA CTG CAA GTG CTG GTC GAT
Val Glu Val Asp Val Ser Ala Ser Ile Thr Leu Gln Val Leu Val Asp
55 60 65

GCC CCA GGG AAC ATT TCC TGT CTC TGG GTC TTT AAG CAC AGC TCC CTG
Ala Pro Gly Asn Ile Ser Cys Leu Trp Val Phe Lys His Ser Ser Leu
70 75 80 85

AAT TGC CAG CCA CAT TTT GAT TTA CAA AAC AGA GGA GTT GTT TCC ATG
Asn Cys Gln Pro His Phe Asp Leu Gln Asn Arg Gly Val Val Ser Met
90 95 100

GTC ATT TTG AAA ATG ACA GAA ACC CAA GCT GGA GAA TAC CTA CTT TTT
Val Ile Leu Lys Met Thr Glu Thr Gln Ala Gly Glu Tyr Leu Leu Phe
105 110 115

ATT CAG AGT GAA GCT ACC AAT TAC ACA ATA TTG TTT ACA GTG AGT ATA
Ile Gln Ser Glu Ala Thr Asn Tyr Thr Ile Leu Phe Thr Val Ser Ile
120 125 130

AGA AAT ACC CTG CTT TAC ACA TTA AGA AGA CCT TAC TTT AGA AAA ATG
Arg Asn Thr Leu Leu Tyr Thr Leu Arg Arg Pro Tyr Phe Arg Lys Met
135 140 145

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Fig. 1b.2

GAA AAC CAG GAC GCC CTG GTC TGC ATA TCT GAG AGC GTT CCA GAG CCG
 Glu Asn Gln Asp Ala Leu Val Cys Ile Ser Glu Ser Val Pro Glu Pro
 150 155 160 165

ATC GTG GAA TGG GTG CTT TGC GAT TCA CAG GGG GAA AGC TGT AAA GAA
 Ile Val Glu Trp Val Leu Cys Asp Ser Gln Gly Glu Ser Cys Lys Glu
 170 175 180

GAA AGT CCA GCT GTT GTT AAA AAG GAG GAA AAA GTG CTT CAT GAA TTA
 Glu Ser Pro Ala Val Val Lys Lys Glu Glu Lys Val Leu His Glu Leu
 185 190 195

TTT GGG ACG GAC ATA AGG TGC TGT GCC AGA AAT GAA CTG GGC AGG GAA
 Phe Gly Thr Asp Ile Arg Cys Cys Ala Arg Asn Glu Leu Gly Arg Glu
 200 205 210

TGC ACC AGG CTG TTC ACA ATA GAT CTA AAT CAA ACT CCT CAG ACC ACA
 Cys Thr Arg Leu Phe Thr Ile Asp Leu Asn Gln Thr Pro Gln Thr Thr
 215 220 225

TTG CCA CAA TTA TTT CTT AAA GTA GGG GAA CCC TTA TGG ATA AGG TGC
 Leu Pro Gln Leu Phe Leu Lys Val Gly Glu Pro Leu Trp Ile Arg Cys
 230 235 240 245

AAA GCT GTT CAT GTG AAC CAT GGA TTC GGG CTC ACC TGG GAA TTA GAA
 Lys Ala Val His Val Asn His Gly Phe Gly Leu Thr Trp Glu Leu Glu
 250 255 260

AAC AAA GCA CTC GAG GAG GGC AAC TAC TTT GAG ATG AGT ACC TAT TCA
 Asn Lys Ala Leu Glu Glu Gly Asn Tyr Phe Glu Met Ser Thr Tyr Ser
 265 270 275

ACA AAC AGA ACT ATG ATA CGG ATT CTG TTT GCT TTT GTA TCA TCA GTG
 Thr Asn Arg Thr Met Ile Arg Ile Leu Phe Ala Phe Val Ser Ser Val
 280 285 290

GCA AGA AAC GAC ACC GGA TAC TAC ACT TGT TCC TCT TCA AAG CAT CCC
 Ala Arg Asn Asp Thr Gly Tyr Tyr Thr Cys Ser Ser Ser Lys His Pro
 295 300 305

AGT CAA TCA GCT TTG GTT ACC ATC GTA GGA AAG GGA TTT ATA AAT GCT
 Ser Gln Ser Ala Leu Val Thr Ile Val Gly Lys Gly Phe Ile Asn Ala
 310 315 320 325

ACC AAT TCA AGT GAA GAT TAT GAA ATT GAC CAA TAT GAA GAG TTT TGT
 Thr Asn Ser Ser Glu Asp Tyr Glu Ile Asp Gln Tyr Glu Glu Phe Cys
 330 335 340

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Fig. 1b.3

TTT	TCT	GTC	AGG	TTT	AAA	GCC	TAC	CCA	CAA	ATC	AGA	TGT	ACG	TGG	ACC	
Phe	Ser	Val	Arg	Phe	Lys	Ala	Tyr	Pro	Gln	Ile	Arg	Cys	Thr	Trp	Thr	
			345					350					355			
TTC	TCT	CGA	AAA	TCA	TTT	CCT	TGT	GAG	CAA	AAG	GGT	CTT	GAT	AAC	GGA	
Phe	Ser	Arg	Lys	Ser	Phe	Pro	Cys	Glu	Gln	Lys	Gly	Leu	Asp	Asn	Gly	
		360					365					370				
TAC	AGC	ATA	TCC	AAG	TTT	TGC	AAT	CAT	AAG	CAC	CAG	CCA	GGA	GAA	TAT	
Tyr	Ser	Ile	Ser	Lys	Phe	Cys	Asn	His	Lys	His	Gln	Pro	Gly	Glu	Tyr	
	375					380					385					
ATA	TTC	CAT	GCA	GAA	AAT	GAT	GAT	GCC	CAA	TTT	ACC	AAA	ATG	TTC	ACG	
Ile	Phe	His	Ala	Glu	Asn	Asp	Asp	Ala	Gln	Phe	Thr	Lys	Met	Phe	Thr	
390					395					400					405	
CTG	AAT	ATA	AGA	AGG	AAA	CCT	CAA	GTG	CTC	GCA	GAA	GCA	TCG	GCA	AGT	
Leu	Asn	Ile	Arg	Arg	Lys	Pro	Gln	Val	Leu	Ala	Glu	Ala	Ser	Ala	Ser	
			410					415						420		
CAG	GCG	TCC	TGT	TTC	TCG	GAT	GGA	TAC	CCA	TTA	CCA	TCT	TGG	ACC	TGG	
Gln	Ala	Ser	Cys	Phe	Ser	Asp	Gly	Tyr	Pro	Leu	Pro	Ser	Trp	Thr	Trp	
			425					430					435			
AAG	AAG	TGT	TCA	GAC	AAG	TCT	CCC	AAC	TGC	ACA	GAA	GAG	ATC	ACA	GAA	
Lys	Lys	Cys	Ser	Asp	Lys	Ser	Pro	Asn	Cys	Thr	Glu	Glu	Ile	Thr	Glu	
		440					445					450				
GGA	GTC	TGG	AAT	AGA	AAG	GCT	AAC	AGA	AAA	GTG	TTT	GGA	CAG	TGG	GTG	
Gly	Val	Trp	Asn	Arg	Lys	Ala	Asn	Arg	Lys	Val	Phe	Gly	Gln	Trp	Val	
	455					460					465					
TCG	AGC	AGT	ACT	CTA	AAC	ATG	AGT	GAA	GCC	ATA	AAA	GGG	TTC	CTG	GTC	
Ser	Ser	Ser	Thr	Leu	Asn	Met	Ser	Glu	Ala	Ile	Lys	Gly	Phe	Leu	Val	
470					475					480					485	
AAG	TGC	TGT	GCA	TAC	AAT	TCC	CTT	GGC	ACA	TCT	TGT	GAG	ACG	ATC	CTT	
Lys	Cys	Cys	Ala	Tyr	Asn	Ser	Leu	Gly	Thr	Ser	Cys	Glu	Thr	Ile	Leu	
			490					495						500		
TTA	AAC	TCT	CCA	GGC	CCC	TTC	CCT	TTC	ATC	CAA	GAC	AAC	ATC	TCA	TTC	
Leu	Asn	Ser	Pro	Gly	Pro	Phe	Pro	Phe	Ile	Gln	Asp	Asn	Ile	Ser	Phe	
			505					510						515		
TAT	GCA	ACA	ATT	GGT	GTT	TGT	CTC	CTC	TTC	ATT	GTC	GTT	TTA	ACC	CTG	
Tyr	Ala	Thr	Ile	Gly	Val	Cys	Leu	Leu	Phe	Ile	Val	Val	Leu	Thr	Leu	
		520					525					530				

Fig. 1b.5

TCA	GGG	CTT	CAT	GGG	AAT	TCA	TTT	CAC	TCT	GAA	GAT	GAA	ATT	GAA	TAT	
Ser	Gly	Leu	His	Gly	Asn	Ser	Phe	His	Ser	Glu	Asp	Glu	Ile	Glu	Tyr	
				730					735					740		
GAA	AAC	CAA	AAA	AGG	CTG	GAA	GAA	GAG	GAG	GAC	TTG	AAT	GTG	CTT	ACA	
Glu	Asn	Gln	Lys	Arg	Leu	Glu	Glu	Glu	Glu	Asp	Leu	Asn	Val	Leu	Thr	
			745					750					755			
TTT	GAA	GAT	CTT	CTT	TGC	TTT	GCA	TAT	CAA	GTT	GCC	AAA	GGA	ATG	GAA	
Phe	Glu	Asp	Leu	Leu	Cys	Phe	Ala	Tyr	Gln	Val	Ala	Lys	Gly	Met	Glu	
		760					765					770				
TTT	CTG	GAA	TTT	AAG	TCG	TGT	GTT	CAC	AGA	GAC	CTG	GCC	GCC	AGG	AAC	
Phe	Leu	Glu	Phe	Lys	Ser	Cys	Val	His	Arg	Asp	Leu	Ala	Ala	Arg	Asn	
	775					780					785					
GTG	CTT	GTC	ACC	CAC	GGG	AAA	GTG	GTG	AAG	ATA	TGT	GAC	TTT	GGA	TTG	
Val	Leu	Val	Thr	His	Gly	Lys	Val	Val	Lys	Ile	Cys	Asp	Phe	Gly	Leu	
	790				795					800					805	
GCT	CGA	GAT	ATC	ATG	AGT	GAT	TCC	AAC	TAT	GTT	GTC	AGG	GGC	AAT	GCC	
Ala	Arg	Asp	Ile	Met	Ser	Asp	Ser	Asn	Tyr	Val	Val	Arg	Gly	Asn	Ala	
				810					815					820		
CGT	CTG	CCT	GTA	AAA	TGG	ATG	GCC	CCC	GAA	AGC	CTG	TTT	GAA	GGC	ATC	
Arg	Leu	Pro	Val	Lys	Trp	Met	Ala	Pro	Glu	Ser	Leu	Phe	Glu	Gly	Ile	
			825					830					835			
TAC	ACC	ATT	AAG	AGT	GAT	GTC	TGG	TCA	TAT	GGA	ATA	TTA	CTG	TGG	GAA	
Tyr	Thr	Ile	Lys	Ser	Asp	Val	Trp	Ser	Tyr	Gly	Ile	Leu	Leu	Trp	Glu	
		840					845					850				
ATC	TTC	TCA	CTT	GGT	GTG	AAT	CCT	TAC	CCT	GGC	ATT	CCG	GTT	GAT	GCT	
Ile	Phe	Ser	Leu	Gly	Val	Asn	Pro	Tyr	Pro	Gly	Ile	Pro	Val	Asp	Ala	
	855					860					865					
AAC	TTC	TAC	AAA	CTG	ATT	CAA	AAT	GGA	TTT	AAA	ATG	GAT	CAG	CCA	TTT	
Asn	Phe	Tyr	Lys	Leu	Ile	Gln	Asn	Gly	Phe	Lys	Met	Asp	Gln	Pro	Phe	
	870				875					880					885	
TAT	GCT	ACA	GAA	GAA	ATA	TAC	ATT	ATA	ATG	CAA	TCC	TGC	TGG	GCT	TTT	
Tyr	Ala	Thr	Glu	Glu	Ile	Tyr	Ile	Ile	Met	Gln	Ser	Cys	Trp	Ala	Phe	
			890						895					900		
GAC	TCA	AGG	AAA	CGG	CCA	TCC	TTC	CCT	AAT	TTG	ACT	TCG	TTT	TTA	GGA	
Asp	Ser	Arg	Lys	Arg	Pro	Ser	Phe	Pro	Asn	Leu	Thr	Ser	Phe	Leu	Gly	
			905					910					915			

Fig. 1b.6

TGT CAG CTG GCA GAT GCA GAA GAA GCG ATG TAT CAG AAT GTG GAT GGC
 Cys Gln Leu Ala Asp Ala Glu Glu Ala Met Tyr Gln Asn Val Asp Gly
 920 925 930

CGT GTT TCG GAA TGT CCT CAC ACC TAC CAA AAC AGG CGA CCT TTC AGC
 Arg Val Ser Glu Cys Pro His Thr Tyr Gln Asn Arg Arg Pro Phe Ser
 935 940 945

AGA GAG ATG GAT TTG GGG CTA CTC TCT CCG CAG GCT CAG GTC GAA GAT
 Arg Glu Met Asp Leu Gly Leu Leu Ser Pro Gln Ala Gln Val Glu Asp
 950 955 960 965

TCG TAGAGGAACA ATTTAGTTTT AAGGACTTCA TCCCTCCACC TATCCCTAAC
 Ser

AGGCTGTAGA TTACCAAAC AAGATTAATT TCATCACTAA AAGAAAATCT ATTATCAACT
 GCTGCTTCAC CAGACTTTTC TCTAGAAGCC GTCTGCGTTT ACTCTTGTTT TCAAAGGGAC
 TTTTGTA AAA TCAAATCATC CTGTCACAAG GCAGGAGGAG CTGATAATGA ACTTTATTGG
 AGCATTGATC TGCATCCAAG GCCTTCTCAG GCCGGCTTGA GTGAATTGTG TACCTGAAGT
 ACAGTATATT CTTGTAAATA CATAAAACAA AAGCATTTTG CTAAGGAGAA GCTAATATGA
 TTTTTTAAGT CTATGTTTTA AAATAATATG TAAATTTTTC AGCTATTTAG TGATATATTT
 TATGGGTGGG AATAAAATTT CTA CTACTACAGA AAAAAAAAAA AAAAAAAAAA AAAAA

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 2046T550
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 4046T550
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 96046T550
 97046T550
 98046T550
 99046T550
 100046T550

Fig. 2.1

CTGTGTCCCG CAGCCGGATA ACCTGGCTGA CCCGATTCCG CGGACACCCG TGCAGCCGCG
 GCTGGAGCCA GGGCGCCGGT GCCCGCGCTC TCCCCGGTCT TGCCTGCGG GGGCCGATAC
 CGCCTCTGTG ACTTCTTTGC GGGCCAGGGA CGGAGAAGGA GTCTGTGCCT GAGAACTGG
 GCTCTGTGCC CAGGCGCGAG GTGCAGG ATG GAG AGC AAG GGC CTG CTA GCT
 Met Glu Ser Lys Gly Leu Leu Ala
 -19 -15

GTC GCT CTG TGG TTC TGC GTG GAG ACC CGA GCC GCC TCT GTG GGT TTG
 Val Ala Leu Trp Phe Cys Val Glu Thr Arg Ala Ala Ser Val Gly Leu
 -10 -5 1 5

CCT GGC GAT TTT CTC CAT CCC CCC AAG CTC AGC ACA CAG AAA GAC ATA
 Pro Gly Asp Phe Leu His Pro Pro Lys Leu Ser Thr Gln Lys Asp Ile
 10 15 20

CTG ACA ATT TTG GCA AAT ACA ACC CTT CAG ATT ACT TGC AGG GGA CAG
 Leu Thr Ile Leu Ala Asn Thr Thr Leu Gln Ile Thr Cys Arg Gly Gln
 25 30 35

CGG GAC CTG GAC TGG CTT TGG CCC AAT GCT CAG CGT GAT TCT GAG GAA
 Arg Asp Leu Asp Trp Leu Trp Pro Asn Ala Gln Arg Asp Ser Glu Glu
 40 45 50

AGG GTA TTG GTG ACT GAA TGC GGC GGT GGT GAC AGT ATC TTC TGC AAA
 Arg Val Leu Val Thr Glu Cys Gly Gly Gly Asp Ser Ile Phe Cys Lys
 55 60 65

ACA CTC ACC ATT CCC AGG GTG GTT GGA AAT GAT ACT GGA GCC TAC AAG
 Thr Leu Thr Ile Pro Arg Val Val Gly Asn Asp Thr Gly Ala Tyr Lys
 70 75 80 85

TGC TCG TAC CGG GAC GTC GAC ATA GCC TCC ACT GTT TAT GTC TAT GTT
 Cys Ser Tyr Arg Asp Val Asp Ile Ala Ser Thr Val Tyr Val Tyr Val
 90 95 100

CGA GAT TAC AGA TCA CCA TTC ATC GCC TCT GTC AGT GAC CAG CAT GGC
 Arg Asp Tyr Arg Ser Pro Phe Ile Ala Ser Val Ser Asp Gln His Gly
 105 110 115

ATC GTG TAC ATC ACC GAG AAC AAG AAC AAA ACT GTG GTG ATC CCC TGC
 Ile Val Tyr Ile Thr Glu Asn Lys Asn Lys Thr Val Val Ile Pro Cys
 120 125 130

Fig. 2.3

ACA Thr	GTG Val	GGC Gly	AGT Ser	CAA Gln 330	GTC Val	CGA Arg	ATC Ile	CCT Pro	GTG Val 335	AAG Lys	TAT Tyr	CTC Leu	AGT Ser	TAC Tyr 340	CCA Pro
GCT Ala	CCT Pro	GAT Asp	ATC Ile 345	AAA Lys	TGG Trp	TAC Tyr	AGA Arg	AAT Asn 350	GGA Gly	AGG Arg	CCC Pro	ATT Ile	GAG Glu 355	TCC Ser	AAC Asn
TAC Tyr	ACA Thr	ATG Met 360	ATT Ile	GTT Val	GGC Gly	GAT Asp	GAA Glu 365	CTC Leu	ACC Thr	ATC Ile	ATG Met	GAA Glu 370	GTG Val	ACT Thr	GAA Glu
AGA Arg	GAT Asp 375	GCA Ala	GGA Gly	AAC Asn	TAC Tyr	ACG Thr 380	GTC Val	ATC Ile	CTC Leu	ACC Thr	AAC Asn 385	CCC Pro	ATT Ile	TCA Ser	ATG Met
GAG Glu 390	AAA Lys	CAG Gln	AGC Ser	CAC His	ATG Met 395	GTC Val	TCT Ser	CTG Leu	GTT Val	GTG Val 400	AAT Asn	GTC Val	CCA Pro	CCC Pro	CAG Gln 405
ATC Ile	GGT Gly	GAG Glu	AAA Lys	GCC Ala 410	TTG Leu	ATC Ile	TCG Ser	CCT Pro	ATG Met 415	GAT Asp	TCC Ser	TAC Tyr	CAG Gln 420	TAT Tyr	GGG Gly
ACC Thr	ATG Met	CAG Gln	ACA Thr 425	TTG Leu	ACA Thr	TGC Cys	ACA Thr	GTC Val 430	TAC Tyr	GCC Ala	AAC Asn	CCT Pro	CCC Pro 435	CTG Leu	CAC His
CAC His	ATC Ile	CAG Gln 440	TGG Trp	TAC Tyr	TGG Trp	CAG Gln	CTA Leu 445	GAA Glu	GAA Glu	GCC Ala	TGC Cys	TCC Ser 450	TAC Tyr	AGA Arg	CCC Pro
GGC Gly	CAA Gln 455	ACA Thr	AGC Ser	CCG Pro	TAT Tyr	GCT Ala 460	TGT Cys	AAA Lys	GAA Glu	TGG Trp	AGA Arg 465	CAC His	GTG Val	GAG Glu	GAT Asp
TTC Phe 470	CAG Gln	GGG Gly	GGA Gly	AAC Asn	AAG Lys 475	ATC Ile	GAA Glu	GTC Val	ACC Thr	AAA Lys 480	AAC Asn	CAA Gln	TAT Tyr	GCC Ala	CTG Leu 485
ATT Ile	GAA Glu	GGA Gly	AAA Lys	AAC Asn 490	AAA Lys	ACT Thr	GTA Val	AGT Ser	ACG Thr 495	CTG Leu	GTC Val	ATC Ile	CAA Gln	GCT Ala 500	GCC Ala
AAC Asn	GTG Val	TCA Ser	GCG Ala 505	TTG Leu	TAC Tyr	AAA Lys	TGT Cys	GAA Glu 510	GCC Ala	ATC Ile	AAC Asn	AAA Lys	GCG Ala 515	GGA Gly	CGA Arg

Fig. 2.4

GGA	GAG	AGG	GTC	ATC	TCC	TTC	CAT	GTG	ATC	AGG	GGT	CCT	GAA	ATT	ACT	
Gly	Glu	Arg	Val	Ile	Ser	Phe	His	Val	Ile	Arg	Gly	Pro	Glu	Ile	Thr	
		520					525					530				
GTG	CAA	CCT	GCT	GCC	CAG	CCA	ACT	GAG	CAG	GAG	AGT	GTG	TCC	CTG	TTG	
Val	Gln	Pro	Ala	Ala	Gln	Pro	Thr	Glu	Gln	Glu	Ser	Val	Ser	Leu	Leu	
	535					540					545					
TGC	ACT	GCA	GAC	AGA	AAT	ACG	TTT	GAG	AAC	CTC	ACG	TGG	TAC	AAG	CTT	
Cys	Thr	Ala	Asp	Arg	Asn	Thr	Phe	Glu	Asn	Leu	Thr	Trp	Tyr	Lys	Leu	
	550				555					560					565	
GGC	TCA	CAG	GCA	ACA	TCG	GTC	CAC	ATG	GGC	GAA	TCA	CTC	ACA	CCA	GTT	
Gly	Ser	Gln	Ala	Thr	Ser	Val	His	Met	Gly	Glu	Ser	Leu	Thr	Pro	Val	
				570					575					580		
TGC	AAG	AAC	TTG	GAT	GCT	CTT	TGG	AAA	CTG	AAT	GGC	ACC	ATG	TTT	TCT	
Cys	Lys	Asn	Leu	Asp	Ala	Leu	Trp	Lys	Leu	Asn	Gly	Thr	Met	Phe	Ser	
			585					590					595			
AAC	AGC	ACA	AAT	GAC	ATC	TTG	ATT	GTG	GCA	TTT	CAG	AAT	GCC	TCT	CTG	
Asn	Ser	Thr	Asn	Asp	Ile	Leu	Ile	Val	Ala	Phe	Gln	Asn	Ala	Ser	Leu	
		600					605					610				
CAG	GAC	CAA	GGC	GAC	TAT	GTT	TGC	TCT	GCT	CAA	GAT	AAG	AAG	ACC	AAG	
Gln	Asp	Gln	Gly	Asp	Tyr	Val	Cys	Ser	Ala	Gln	Asp	Lys	Lys	Thr	Lys	
	615					620					625					
AAA	AGA	CAT	TGC	CTG	GTC	AAA	CAG	CTC	ATC	ATC	CTA	GAG	CGC	ATG	GCA	
Lys	Arg	His	Cys	Leu	Val	Lys	Gln	Leu	Ile	Ile	Leu	Glu	Arg	Met	Ala	
	630				635					640					645	
CCC	ATG	ATC	ACC	GGA	AAT	CTG	GAG	AAT	CAG	ACA	ACA	ACC	ATT	GGC	GAG	
Pro	Met	Ile	Thr	Gly	Asn	Leu	Glu	Asn	Gln	Thr	Thr	Thr	Ile	Gly	Glu	
				650					655					660		
ACC	ATT	GAA	GTG	ACT	TGC	CCA	GCA	TCT	GGA	AAT	CCT	ACC	CCA	CAC	ATT	
Thr	Ile	Glu	Val	Thr	Cys	Pro	Ala	Ser	Gly	Asn	Pro	Thr	Pro	His	Ile	
			665					670					675			
ACA	TGG	TTC	AAA	GAC	AAC	GAG	ACC	CTG	GTA	GAA	GAT	TCA	GGC	ATT	GTA	
Thr	Trp	Phe	Lys	Asp	Asn	Glu	Thr	Leu	Val	Glu	Asp	Ser	Gly	Ile	Val	
		680					685					690				
CTG	AGA	GAT	GGG	AAC	CGG	AAC	CTG	ACT	ATC	CGC	AGG	GTG	AGG	AAG	GAG	
Leu	Arg	Asp	Gly	Asn	Arg	Asn	Leu	Thr	Ile	Arg	Arg	Val	Arg	Lys	Glu	
	695					700					705					

Fig. 2.5

GAT Asp 710	GGA Gly	GGC Gly	CTC Leu	TAC Tyr	ACC Thr 715	TGC Cys	CAG Gln	GCC Ala	TGC Cys	AAT Asn 720	GTC Val	CTT Leu	GGC Gly	TGT Cys 725	GCA Ala
AGA Arg	GCG Ala	GAG Glu	ACG Thr	CTC Leu 730	TTC Phe	ATA Ile	ATA Ile	GAA Glu	GGT Gly 735	GCC Ala	CAG Gln	GAA Glu	AAG Lys	ACC Thr 740	AAC Asn
TTG Leu	GAA Glu	GTC Val	ATT Ile 745	ATC Ile	CTC Leu	GTC Val	GGC Gly	ACT Thr 750	GCA Ala	GTG Val	ATT Ile	GCC Ala	ATG Met 755	TTC Phe	TTC Phe
TGG Trp	CTC Leu	CTT Leu 760	CTT Leu	GTC Val	ATT Ile	CTC Leu	GTA Val 765	CGG Arg	ACC Thr	GTT Val	AAG Lys	CGG Arg 770	GCC Ala	AAT Asn	GAA Glu
GGG Gly 775	GAA Glu	CTG Leu	AAG Lys	ACA Thr	GGC Gly	TAC Tyr 780	TTG Leu	TCT Ser	ATT Ile	GTC Val	ATG Met 785	GAT Asp	CCA Pro	GAT Asp	GAA Glu
TTG Leu 790	CCC Pro	TTG Leu	GAT Asp	GAG Glu	CGC Arg 795	TGT Cys	GAA Glu	CGC Arg	TTG Leu	CCT Pro 800	TAT Tyr	GAT Asp	GCC Ala	AGC Ser	AAG Lys 805
TGG Trp	GAA Glu	TTC Phe	CCC Pro	AGG Arg 810	GAC Asp	CGG Arg	CTG Leu	AAA Lys	CTA Leu 815	GGA Gly	AAA Lys	CCT Pro	CTT Leu	GGC Gly 820	CGC Arg
GGT Gly	GCC Ala	TTC Phe	GGC Gly 825	CAA Gln	GTG Val	ATT Ile	GAG Glu	GCA Ala 830	GAC Asp	GCT Ala	TTT Phe	GGA Gly	ATT Ile 835	GAC Asp	AAG Lys
ACA Thr	GCG Ala	ACT Thr	TGC Cys	AAA Lys	ACA Thr	GTA Val	GCC Ala 845	GTC Val	AAG Lys	ATG Met	TTG Leu	AAA Lys 850	GAA Glu	GGA Gly	GCA Ala
ACA Thr 855	CAC His	AGC Ser	GAG Glu	CAT His	CGA Arg	GCC Ala 860	CTC Leu	ATG Met	TCT Ser	GAA Glu	CTC Leu 865	AAG Lys	ATC Ile	CTC Leu	ATC Ile
CAC His 870	ATT Ile	GGT Gly	CAC His	CAT His	CTC Leu 875	AAT Asn	GTG Val	GTG Val	AAC Asn	CTC Leu 880	CTA Leu	GGC Gly	GCC Ala	TGC Cys	ACC Thr 885
AAG Lys	CCG Pro	GGA Gly	GGG Gly	CCT Pro 890	CTC Leu	ATG Met	GTG Val	ATT Ile	GTG Val 895	GAA Glu	TTC Phe	TCG Ser	AAG Lys	TTT Phe 900	GGA Gly

Fig. 2.6

AAC CTA TCA ACT TAC TTA CGG GGC AAG AGA AAT GAA TTT GTT CCC TAT
 Asn Leu Ser Thr Tyr Leu Arg Gly Lys Arg Asn Glu Phe Val Pro Tyr
 905 910 915

AAG AGC AAA GGG GCA CGC TTC CGC CAG GGC AAG GAC TAC GTT GGG GAG
 Lys Ser Lys Gly Ala Arg Phe Arg Gln Gly Lys Asp Tyr Val Gly Glu
 920 925 930

CTC TCC GTG GAT CTG AAA AGA CGC TTG GAC AGC ATC ACC AGC AGC CAG
 Leu Ser Val Asp Leu Lys Arg Arg Leu Asp Ser Ile Thr Ser Ser Gln
 935 940 945

AGC TCT GCC AGC TCA GGC TTT GTT GAG GAG AAA TCG CTC AGT GAT GTA
 Ser Ser Ala Ser Ser Gly Phe Val Glu Glu Lys Ser Leu Ser Asp Val
 950 955 960 965

GAG GAA GAA GAA GCT TCT GAA GAA CTG TAC AAG GAC TTC CTG ACC TTG
 Glu Glu Glu Glu Ala Ser Glu Glu Leu Tyr Lys Asp Phe Leu Thr Leu
 970 975 980

GAG CAT CTC ATC TGT TAC AGC TTC CAA GTG GCT AAG GGC ATG GAG TTC
 Glu His Leu Ile Cys Tyr Ser Phe Gln Val Ala Lys Gly Met Glu Phe
 985 990 995

TTG GCA TCA AGG AAG TGT ATC CAC AGG GAC CTG GCA GCA CGA AAC ATT
 Leu Ala Ser Arg Lys Cys Ile His Arg Asp Leu Ala Ala Arg Asn Ile
 1000 1005 1010

CTC CTA TCG GAG AAG AAT GTG GTT AAG ATC TGT GAC TTC GGC TTG GCC
 Leu Leu Ser Glu Lys Asn Val Val Lys Ile Cys Asp Phe Gly Leu Ala
 1015 1020 1025

CGG GAC ATT TAT AAA GAC CCG GAT TAT GTC AGA AAA GGA GAT GCC CGA
 Arg Asp Ile Tyr Lys Asp Pro Asp Tyr Val Arg Lys Gly Asp Ala Arg
 1030 1035 1040 1045

CTC CCT TTG AAG TGG ATG GCC CCG GAA ACC ATT TTT GAC AGA GTA TAC
 Leu Pro Leu Lys Trp Met Ala Pro Glu Thr Ile Phe Asp Arg Val Tyr
 1050 1055 1060

ACA ATT CAG AGC GAT GTG TGG TCT TTC GGT GTG TTG CTC TGG GAA ATA
 Thr Ile Gln Ser Asp Val Trp Ser Phe Gly Val Leu Leu Trp Glu Ile
 1065 1070 1075

TTT TCC TTA GGT GCC TCC CCA TAC CCT GGG GTC AAG ATT GAT GAA GAA
 Phe Ser Leu Gly Ala Ser Pro Tyr Pro Gly Val Lys Ile Asp Glu Glu
 1080 1085 1090

09019408.0404

Fig. 2.7

TTT	TGT	AGG	AGA	TTG	AAA	GAA	GGA	ACT	AGA	ATG	CGG	GCT	CCT	GAC	TAC	
Phe	Cys	Arg	Arg	Leu	Lys	Glu	Gly	Thr	Arg	Met	Arg	Ala	Pro	Asp	Tyr	
	1095						1100					1105				
ACT	ACC	CCA	GAA	ATG	TAC	CAG	ACC	ATG	CTG	GAC	TGC	TGG	CAT	GAG	GAC	
Thr	Thr	Pro	Glu	Met	Tyr	Gln	Thr	Met	Leu	Asp	Cys	Trp	His	Glu	Asp	
	1110					1115					1120				1125	
CCC	AAC	CAG	AGA	CCC	TCG	TTT	TCA	GAG	TTG	GTG	GAG	CAT	TTG	GGA	AAC	
Pro	Asn	Gln	Arg	Pro	Ser	Phe	Ser	Glu	Leu	Val	Glu	His	Leu	Gly	Asn	
				1130					1135					1140		
CTC	CTG	CAA	GCA	AAT	GCG	CAG	CAG	GAT	GGC	AAA	GAC	TAT	ATT	GTT	CTT	
Leu	Leu	Gln	Ala	Asn	Ala	Gln	Gln	Asp	Gly	Lys	Asp	Tyr	Ile	Val	Leu	
			1145					1150					1155			
CCA	ATG	TCA	GAG	ACA	CTG	AGC	ATG	GAA	GAG	GAT	TCT	GGA	CTC	TCC	CTG	
Pro	Met	Ser	Glu	Thr	Leu	Ser	Met	Glu	Glu	Asp	Ser	Gly	Leu	Ser	Leu	
		1160					1165					1170				
CCT	ACC	TCA	CCT	GTT	TCC	TGT	ATG	GAG	GAA	GAG	GAA	GTG	TGC	GAC	CCC	
Pro	Thr	Ser	Pro	Val	Ser	Cys	Met	Glu	Glu	Glu	Glu	Val	Cys	Asp	Pro	
	1175					1180						1185				
AAA	TTC	CAT	TAT	GAC	AAC	ACA	GCA	GGA	ATC	AGT	CAT	TAT	CTC	CAG	AAC	
Lys	Phe	His	Tyr	Asp	Asn	Thr	Ala	Gly	Ile	Ser	His	Tyr	Leu	Gln	Asn	
	1190					1195				1200					1205	
AGT	AAG	CGA	AAG	AGC	CGG	CCA	GTG	AGT	GTA	AAA	ACA	TTT	GAA	GAT	ATC	
Ser	Lys	Arg	Lys	Ser	Arg	Pro	Val	Ser	Val	Lys	Thr	Phe	Glu	Asp	Ile	
				1210					1215					1220		
CCA	TTG	GAG	GAA	CCA	GAA	GTA	AAA	GTG	ATC	CCA	GAT	GAC	AGC	CAG	ACA	
Pro	Leu	Glu	Glu	Pro	Glu	Val	Lys	Val	Ile	Pro	Asp	Asp	Ser	Gln	Thr	
			1225				1230						1235			
GAC	AGT	GGG	ATG	GTC	CTT	GCA	TCA	GAA	GAG	CTG	AAA	ACT	CTG	GAA	GAC	
Asp	Ser	Gly	Met	Val	Leu	Ala	Ser	Glu	Glu	Leu	Lys	Thr	Leu	Glu	Asp	
		1240					1245					1250				
AGG	AAC	AAA	TTA	TCT	CCA	TCT	TTT	GGT	GGA	ATG	ATG	CCC	AGT	AAA	AGC	
Arg	Asn	Lys	Leu	Ser	Pro	Ser	Phe	Gly	Gly	Met	Met	Pro	Ser	Lys	Ser	
	1255					1260					1265					
AGG	GAG	TCT	GTG	GCC	TCG	GAA	GGC	TCC	AAC	CAG	ACC	AGT	GGC	TAC	CAG	
Arg	Glu	Ser	Val	Ala	Ser	Glu	Gly	Ser	Asn	Gln	Thr	Ser	Gly	Tyr	Gln	
	1270					1275				1280					1285	

Fig. 2.8

TCT GGG TAT CAC TCA GAT GAC ACA GAC ACC ACC GTG TAC TCC AGC GAC
 Ser Gly Tyr His Ser Asp Asp Thr Asp Thr Thr Val Tyr Ser Ser Asp
 1290 1295 1300

GAG GCA GGA CTT TTA AAG ATG GTG GAT GCT GCA GTT CAC GCT GAC TCA
 Glu Ala Gly Leu Leu Lys Met Val Asp Ala Ala Val His Ala Asp Ser
 1305 1310 1315

GGG ACC ACA CTG CAG CTC ACC TCC TGT TTA AAT GGA AGT GGT CCT GTC
 Gly Thr Thr Leu Gln Leu Thr Ser Cys Leu Asn Gly Ser Gly Pro Val
 1320 1325 1330

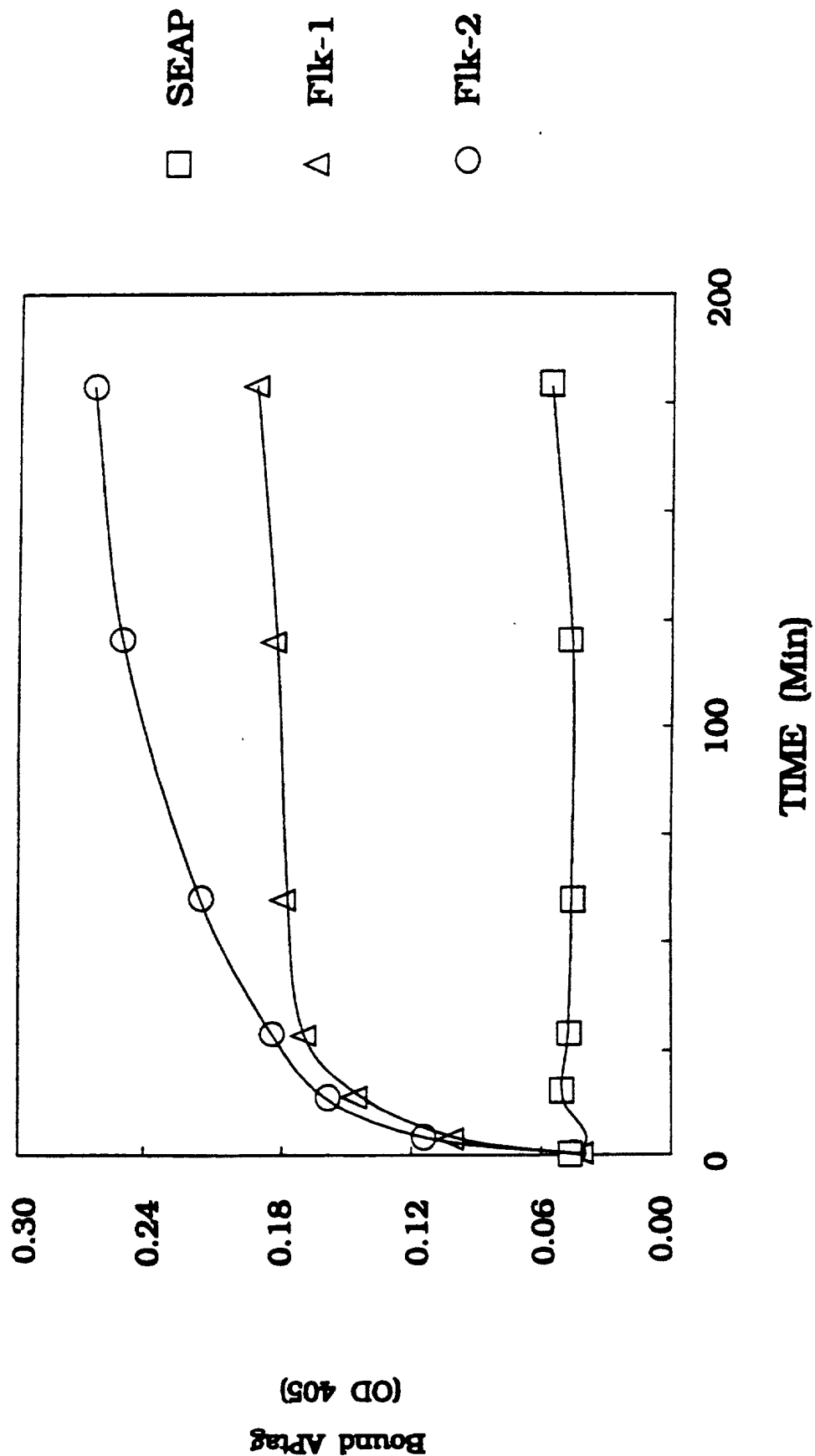
CCG GCT CCG CCC CCA ACT CCT GGA AAT CAC GAG AGA GGT GCT GCT TAG
 Pro Ala Pro Pro Pro Thr Pro Gly Asn His Glu Arg Gly Ala Ala
 1335 1340 1345

ATTTTCAAGT GTTGTTCCTTT CCACCACCCG GAAGTAGCCA CATTTGATTT TCATTTTGG
 AGGAGGGACC TCAGACTGCA AGGAGCTTGT CCTCAGGGCA TTTCCAGAGA AGATGCCCAT
 GACCCAAGAA TGTGTTGACT CTACTCTCTT TTCCATTCAT TTAAAAGTCC TATATAATGT
 GCCCTGCTGT GGTCTCACTA CCAGTTAAAG CAAAAGACTT TCAAACACGT GGACTCTGTC
 CTCCAAGAAG TGGCAACGGC ACCTCTGTGA AACTGGATCG AATGGGCAAT GCTTTGTGTG
 TTGAGGATGG GTGAGATGTC CCAGGGCCGA GTCTGTCTAC CTTGGAGGCT TTGTGGAGGA
 TCGGCTATG AGCCAAGTGT TAAGTGTTGG ATGTGGACTG GGAGGAAGGA AGGCGCAAGC
 CGTCCGAGA GCGGTTGGAG CCTGCAGATG CATTGTGCTG GCTCTGGTGG AGGTGGGCTT
 GTGGCCTGTC AGGAAACGCA AAGGCGGCCG GCAGGGTTTG GTTTTGGAAG GTTTGCGTGC
 TCTTCACAGT CGGGTTACAG GCGAGTTCCC TGTGGCGTTT CCTACTCCTA ATGAGAGTTC
 CTTCCGGACT CTTACGTGTC TCCTGGCCTG GCCCCAGGAA GGAAATGATG CAGCTTGCTC
 CTTCTCATC TCTCAGGCTG TGCCTTAATT CAGAACACCA AAAGAGAGGA ACGTCGGCAG
 AGGCTCCTGA CGGGGCCGAA GAATTGTGAG AACAGAACAG AAATCAGGG TTTCTGCTGG
 GTGGAGACCC ACGTGGCGCC CTGGTGGCAG GTCTGAGGGT TCTCTGTCAA GTGGCGGTAA
 AGGCTCAGGC TGGTGTCTT CCTCTATCTC CACTCCTGTC AGGCCCCCAA GTCTCAGTA
 TTTTAGCTTT GTGGCTTCCT GATGGCAGAA AAATCTTAAT TGGTTGGTTT GCTCTCCAGA

TAATCACTAG CCAGATTTTCG AAATTACTTTT TTAGCCGAGG TTATGATAAC ATCTACTGTA
TCCTTTAGAA TTTTAACCTA TAAAACTATG TCTACTGGTT TCTGCCTGTG TGCTTATGTT
AAAAAAAAAA AAAAA

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FIGURE 3



1/1

FIGURE 4

